The Structure of the Ferric Siderophore Binding Protein FhuD Complexed with Gallichrome

T. Clarke, S. Ku, D. Dougan, H. Vogel, and L. Tari (U. of Calgary) Abstract No. clar1696 Beamline(s): X8C

Introduction: Siderophore binding proteins play a key role in the uptake of iron in many Gram-positive and Gram-negative bacteria. FhuD is a soluble periplasmic binding protein that transports ferrichrome and other hydroxamate siderophores. The crystal structure of FhuD from *Escherichia coli* in complex with the ferrichrome homolog gallichrome has been determined at 1.9 Å resolution, the first structure of aperiplasmic binding protein involved in the uptake of siderophores. Gallichrome is held in a shallow pocket lined with aromatic groups; Arg and Tyr side chains interact directly with the hydroxamate moieties of the siderophore. FhuD possesses a novel fold, suggesting that its mechanisms of ligand binding and release are different from other structurally characterized periplasmic ligand binding proteins.

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References: T.E. Clarke, S.-Y. Ku, D. Dougan, H.J. Vogel, and L.W. Tari, "The Structure of the Ferric Siderophore Binding Protein FhuD complexed with Gallichrome." Nature Struct. Biol. **7**(4), 287, 2000.

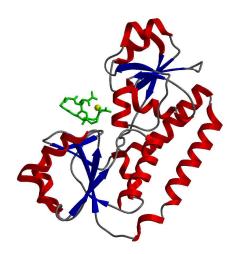


Figure 1. Overall structure of the FhuD-gallichrome complex. The binding cleft is a shallow pocket between the N-terminal and C-terminal domains.